

| Result No. | Score | Query | Match | Length | DB | ID | Description |
|------------|--------|--|-------|--|----------------------|-------------------|---|
| 1 | 1092.5 | Issued_Patents_AA_* | 1: | /cgn2_6/podata/1/1aa/5A_COMB_pep:* | US-09-252-991A-23395 | Sequence 23395, A | Best Local Similarity |
| 2 | 998.5 | Issued_Patents_AA_* | 2: | /cgn2_6/podata/1/1aa/6A_COMB_pep:* | US-09-252-991A-23395 | Sequence 5423, AP | Matches 233; Conservative |
| 3 | 355.6 | Issued_Patents_AA_* | 3: | /cgn2_6/podata/1/1aa/6B_COMB_pep:* | US-09-252-991A-23395 | Sequence 5444, AP | Mismatches 179; |
| 4 | 333.1 | Issued_Patents_AA_* | 4: | /cgn2_6/podata/1/1aa/6B_COMB_pep:* | US-09-252-991A-23395 | Sequence 35, APP1 | Indels 25; |
| 5 | 333.1 | Issued_Patents_AA_* | 5: | /cgn2_6/podata/1/1aa/6C_PCTUS_COMB_pep:* | US-09-252-991A-23395 | Sequence 35, APP1 | Gaps 9; |
| 6 | 333.1 | Issued_Patents_AA_* | 6: | /cgn2_6/podata/1/1aa/backfiles1_pep:* | US-09-252-991A-23395 | Sequence 35, APP1 | |
| 7 | 333.1 | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution. | 7 | 12.0 | 161 | 3 | CURRENT FILING DATE: 1999-02-18 |
| 8 | 110.5 | PREDICTED | 8 | 11.0 | 820 | 4 | PRIOR APPLICATION NUMBER: US 60/074,786 |
| 9 | 11.0 | SUMMARIES | 9 | 11.0 | 709 | 4 | PRIOR FILING DATE: 1998-02-18 |
| 10 | 108.3 | | 10 | 10.0 | 556 | 2 | PRIOR APPLICATION NUMBER: US 60/094,196 |
| 11 | 101.3 | | 11 | 10.0 | 554 | 1 | PRIOR FILING DATE: 1998-07-27 |
| 12 | 100.3 | | 12 | 10.0 | 920 | 3 | NUMBER OF SEQ ID NOS: 33142 |
| 13 | 98.3 | | 13 | 9.5 | 376 | 4 | SEQ ID NO: 23395 |
| 14 | 95.1 | | 14 | 9.5 | 449 | 2 | LENGTH: 529; |
| 15 | 95.1 | | 15 | 9.5 | 449 | 5 | TYPE: PRT |
| 16 | 95.1 | | 16 | 9.5 | 471 | 2 | ORGANISM: Pseudomonas aeruginosa |
| 17 | 95.1 | | 17 | 9.5 | 471 | 5 | RESULT 1 |
| 18 | 95.1 | | 18 | 9.5 | 2662 | 4 | US-09-252-991A-23395 |
| 19 | 94.5 | | 19 | 9.5 | 573 | 4 | US-09-252-991A-28031 |
| 20 | 92.3 | | 20 | 9.2 | 437 | 4 | US-09-252-991A-24355 |
| 21 | 92.3 | | 21 | 9.2 | 459 | 2 | US-09-252-991A-2222-2 |
| 22 | 92.3 | | 22 | 9.2 | 720 | 4 | US-09-252-991A-18618 |
| 23 | 91.3 | | 23 | 9.1 | 571 | 3 | US-09-252-991A-6 |
| 24 | 91.3 | | 24 | 9.1 | 571 | 4 | US-09-252-991A-6 |
| 25 | 91.3 | | 25 | 9.1 | 571 | 4 | US-09-252-991A-6 |
| 26 | 91.3 | | 26 | 9.1 | 571 | 4 | US-09-252-991A-6 |
| 27 | 91.3 | | 27 | 9.1 | 580 | 4 | US-09-252-991A-332 |

ALIGNMENTS

RESULT 1
US-09-252-991A-23395
; Sequence 23395, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: MARC J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196-136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,786
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,196
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 23395
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-23395

Query Match Score 1092.5; DB 4; Length 529;
Best Local Similarity 45.28%; DB 4; Length 529;
Matches 233; Conservative 78; Mismatches 179; Indels 25; Gaps 9;
Qy 13 LVVGDWGLSDQHGNIAKAKTPMDKLCSQNWLQKL-EAHLHVGLPPEGLMGNSEVGHLL 71
Db 24 LILIDGRGHSEPDYNAIYAAKPKVNDRLLATQPHGLJISGSMMDVGLPDGQMGNSEVGHM 83
Qy 72 NIGAGRVTQDITVRNIAVQRNEFTVNPOIVASAERAKKGSSRLHLGLGVSGVSHID 131
Db 84 NIGAGRVTQDITRVKAIIRDFFENPVIAAVDKAVAADKAVHILGLSFGVSHED 143
Qy 132 HLFALIRAFKQOLQVPKVTFTHFADGRTSPGAGYIEQLQFLIASKEYGEATITGRRY 191
Db 144 HLVAMAGMAAKRGAGKYLHATLGDGTPPKSAQPSLERDATTAGLGKGRASITGRRYF 203
Qy 192 AMDRKFWERIKMAYEAIVGGIQKQATVDKAVDVVERAQAQSETDEFLKPIWFSDDG--- 248
Db 204 AMDRNWDRYQAYELJIVDGKAE-FTADDSVAALEAYARGESDEFVKATPVPGAEA 262
Qy 249 -FVKDDDTLIFFNYRADMRQICEUGLERYKDNLSSVPHPMNIQLSG--MTQYKEFP 304
Db 263 VRVEDGDAVINFRADARELSRAFVEPAFNEF---PREAPOLAGFVMITQYAA SIP 318
Qy 305 FSLSEPVTHNVLNLAETLASQVTOFQCAEPKHYTEFFGGREYQFQDERCYWPSP 364
Db 319 APCAFPDEPLTNVGLGYEYLAKHGTQRLIAETSKYAHVTEFFGGREBPEGBRILIPSP 378

RESULT 2
US-09-328-352-5423

; Sequence 5423, Application US/09328352

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC99-03PA

; CURRENT APPLICATION NUMBER: US/09/328, 352

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 8252

; SEQ ID NO: 5423

; LENGTH: 521

; TYPE: PRT

; ORGANISM: Acinetobacter baumannii

Query Match 35.8%; Score 998.5; DB 4; Length 521;
Best Local Similarity 42.2%; pred. No. 1.8e-102; Indels 86; Mismatches 171; Gaps 13;

Query Match 35.6%; Score 992; DB 4; Length 517;
Best Local Similarity 30.2%; pred. No. 9.5e-102; Indels 28; Gaps 8; Mismatches 196;

Query 8 QQKVCLVYIDGWLSDEQHGNATAKAKTPIMDKLCSGNWQK----LEAHGLHYGLPGL 622
Db 15 KQPTALIILDGFAFNRESEIGNAYKQAHKPNDFRY---YEKYPTQIEAQSGLYGLPEQ 700
Query 63 MGNSEVGHMIGAGRIVYQDIVIRINAVORNEFTVNPOQIVASERAKSGRHLGGLVY 122
Db 71 MGNSEVGHMIGAGRIVYQSLTRINKSIEDGEFDNTVLLNTVHKVONGSAHVFGLL 130

Query Match 35.6%; Score 992; DB 4; Length 517;
Best Local Similarity 30.2%; pred. No. 9.5e-102; Indels 28; Gaps 8; Mismatches 196;

Query 13 LVIDWGGLSDEQHGNATAKAKTPIM----DKLCSGNWQKLEAHLGHVLPEGLMG 64
Db 19 LVMDVGHRREATEDNAFLAAKTPNLTAMAKHPNSLISGS----GEDVCPUDGQMG 71

Query 65 NSEYGHMIGAGRIVYQDIVIRINAVORNEFTVNPOQIVASERAKSGRHLGGLVY 124
Db 72 NSEYGHMIGAGRIVYQDFTTRTKDPTGAFHEVLDAVEKAAGAVAHIMGLSEG 131

Query 125 GVHSRIDHFLALIR-AFKQLQPKVFTHFADGRDTSPTSGAGLEQOLQFLASEKY-- 180
Db 132 GVHSIDHIVAMCFLAK--RGKAVYLAHFLGRTDPPRSAQPSLEKIDALFA--KPNQ 187

Query 181 GELATITGRYYAMDRIKWERIKMAYEAIVGGIQKATVDAIVVVVERYAQSETDEFLK 240
Db 188 GRIATMIGRYFAMDRIKRDVRQARLITEGEAVR-TANTAVEGLAYAAANENDEVK 246

Query 241 PIVPSDGKVDDTLIFPFVTHNIALAENLASYQTOQFHCAETEKFYHTFFNGREYOFQ 294
Db 247 ATRIGEIAKVQDGDSVPMFRADRAETRTRAYEVDFKAFGERKVKVQNL-----KPV 299

Query 295 GMTOYNKEFPFSLFPPVTHNIALAENLASYQTOQFHCAETEKFYHTFFNGREYOFQ 354
Db 300 MITYQASIDAPVAMPPELKNSLGEYSSLGRTQLRAETEYAHFTFFSGREDEYP 359

Query 355 DEERCMVPSPKVEATYDLKPKEMNAAGVAKMYQIESGRHPYMCNAPPDMAYHTGKFE 414
Db 360 GEKRILISP-IVATYDLKPKEMSAETYDELKAINSEBDLUVVNVANGDAYHTGVFD 418

Query 415 PAYKACQNTDEAIGKIFERACQTYNYVLMYTSDHGNATEM- IADPGSEHTAHLCNLVFTC 473
Db 419 AAYKAVAEAVDTCLGRVYAVMAKKGHLMTADIGNVEQMDYESGOVHTQHTTLYSF-- 476

Query 474 SSKTFVFKSTPPGDDGERALRDVAPTVLQMLGPVPPENDGVPL 522
Db 477 --IYVGQTAIKAEGG---VLAQAPTILNMQIVPAEMQRNLJ 517

RESULT 4
US-09-328-352-5423

; Sequence 35, Application US/08975762

; Patent No. 620169

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Lodes, Michael J.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/975,762
 FILING DATE: 21-MAR-1997
 TELEPHONE: 206-522-4500

ATTORNEY/AGENT INFORMATION:
 NAME: Maki, David J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 210121.439
 TELECOMMUNICATION INFORMATION:
 CLASSIFICATION: 424
 TELEFAX: 206-682-6031
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 161 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Ehrlichia
 US-08-975-762-35

Query Match 12.0%; Score 333; DB 3; Length 161;
 Best Local Similarity 45.3%; Pred. No. 6.9e-29;
 Matches 72; Conservative 22; Mismatches 61; Indels 4; Gaps 3;

Qy 49 LEAHLHVGVLPEGLMGNSEVGHNLIGAGRIVYQDIVRINLAVQRNEFTNPQIVASAERA 108
 Db 7 LSASGTDVGFLPSGQFNSEVGHISIGCGRIVLDRLRINLEI - NEVHNPKLDFVRDI 64

RESULT 6
 US-09-295-028-35
 Sequence 35, Application US/09295028
 Patent No. 6271381

GENERAL INFORMATION:
 APPLICANT: Houghton, Raymond L.
 INVENTOR: McNeill, Patricia D.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 TITLE OF INVENTION: AND TREATMENT OF EHRLICHIA INFECTION
 FILE REFERENCE: 210121.439c4
 CURRENT APPLICATION NUMBER: US/09/295,028
 CURRENT FILING DATE: 1999-04-20
 NUMBER OF SEQ ID NOS: 85
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 35

LENGTH: 161
 TYPE: PRT
 ORGANISM: Ehrlichia sp.
 US-09-295-028-35

Query Match 12.0%; Score 333; DB 3; Length 161;
 Best Local Similarity 45.3%; Pred. No. 6.9e-29;
 Matches 72; Conservative 22; Mismatches 61; Indels 4; Gaps 3;

Qy 49 LEAHLHVGVLPEGLMGNSEVGHNLIGAGRIVYQDIVRINLAVQRNEFTNPQIVASAERA 108
 Db 7 LSASGTDVGFLPSGQFNSEVGHISIGCGRIVLDRLRINLEI - NEVHNPKLDFVRDI 64

RESULT 5
 US-08-821-324-35
 Sequence 35, Application US/08821324
 Patent No. 6231869

GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 INVENTOR: Lodes, Michael J.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, version #1.30
 CURRENT APPLICATION DATA:

Db 124 GMLNAKI-EHNLNAEATVAGRYAMDRNRLDTCAYD 161

RESULT 7

US-09-106-582-35
Sequence 35, Application US/09106582
; Patent No. 6306102

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Houghton, Raymond

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/106,582

; FILING DATE: 29-JUN-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Maki, David J.

; REGISTRATION NUMBER: 31,392

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 206-622-4900

; TELEFAX: 206-682-6031

; INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 161 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein.

; ORIGINAL SOURCE:

; ORGANISM: *Erlichia*

; US-09-106-582-35

Query Match FILE REFERENCE: 107196_136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIORITY APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIORITY APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO: 32001

; LENGTH: 820

; TYPE: PRT

; ORGANISM: *Pseudomonas aeruginosa*

US-09-252-991A-32001

Query Match Best Local Similarity 20.1%; Score 110.5%; DB 4; Length 820;

Best Local Similarity 20.1%; Pred. No. 0.0099; Matches 60; Mismatches 161; Indels 129; Gaps 18;

Matches 88; Conservative 60; Query 85 RINLAQVNRFV-TNPQIVASA-----

Db 2 KLFIFVVKSSSPHDPRALTAAPSLLADRHAPRLETAQRSGA-----

Db 130 IDHFLALLTRAFTKQLQVPKVFIHEFFADGRDTSPTAGYLEQL-LQFIASEKYGELATIG 188

Db 57 SRVQVLLY-AVDQPQPVPEPFQHAGREQAEEAHAAVYRAQRGQHAEAEIGLVLVG 115

Qy 189 RYAMDRIKRWERIKMAYEAIGGIGOKATDVADYVVERY-----

Db 180 RYAMDRIKRWERIKMAYEAIGGIGOKATDVADYVVERY-----

Db 189 RYAMDRIKRWERIKMAYEAIGGIGOKATDVADYVVERY-----

Db 116 DQJLQIVEDDLQHHVQRVLVE-----

Db 116 DQJLQIVEDDLQHHVQRVLVE-----

Db 116 DQJLQIVEDDLQHHVQRVLVE-----

Db 240 KPTVFSDGKVKDDDTLIFENYFADRMQICEGLGLERYKDLDNLISSVPHPKNLIQSGMTQY 299

Qy 241 KPTVFSDGKVKDDDTLIFENYFADRMQICEGLGLERYKDLDNLISSVPHPKNLIQSGMTQY 299

Db 168 Q-----

RESULT 8

US-09-252-991A-32001

; General Information:

; Applicant: Marc J. Rubenfield et al.

; Title of Invention: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; Title of Invention: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

Query Match FILE REFERENCE: 107196_136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIORITY APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIORITY APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO: 32001

; LENGTH: 820

; TYPE: PRT

; ORGANISM: *Ceanorhabditis elegans*

US-09-668-673B-3

Query Match Sequence 3, Application US/09668673B

; Patent No. 6563956

; General Information:

; Applicant: Emerson, Charles P

; Title of Invention: IDENTIFICATION AND CLONING OF A NEW SUBFAMILY OF

; Title of Invention: SULFATASES AND FUNCTIONAL EMBRYONIC TECHNIQUES FOR

; Title of Invention: CHARACTERIZATION OF SUCH PROTEINS

; File Reference: PENN-0733

; Current Application Number: US/09/668,673B

; Current Filing Date: 2000-09-22

; Prior Application Number: 60/155,738

; Prior Filing Date: 1999-09-23

; Number of Seq ID Nos: 22

; Software: PatentIn Ver. 2.0

; Seq ID No: 3

; Length: 709

; Type: PRT

; Organism: *Ceanorhabditis elegans*

US-09-668-673B-3

Query Match Result 9

US-09-668-673B-3

Query Match Sequence 3, Application US/09668673B

; Patent No. 6563956

; General Information:

; Applicant: Dhoit, Gurjeet K

; Title of Invention: IDENTIFICATION AND CLONING OF A NEW SUBFAMILY OF

; Title of Invention: SULFATASES AND FUNCTIONAL EMBRYONIC TECHNIQUES FOR

; Title of Invention: CHARACTERIZATION OF SUCH PROTEINS

; File Reference: PENN-0733

; Current Application Number: US/09/668,673B

; Current Filing Date: 2000-09-22

; Prior Application Number: 60/155,738

; Prior Filing Date: 1999-09-23

; Number of Seq ID Nos: 22

; Software: PatentIn Ver. 2.0

; Seq ID No: 3

; Length: 709

; Type: PRT

; Organism: *Ceanorhabditis elegans*

US-09-668-673B-3

Query Match Result 8

US-09-668-673B-3

Query Match Sequence 3, Application US/09252991A

; Patent No. 6551795

; General Information:

; Applicant: Marc J. Rubenfield et al.

; Title of Invention: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; Title of Invention: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

Query Match Score 110; DB 4; Length 709;
 Best Local Similarity 22.1%; Pred. No. 0.0087;
 Matches 82; Conservative 45; Mismatches 144; Indels 100; Gaps 20;

REF ID: QY213

Query 213 IGQKATVDKAVDVVERYAQOSETDEFLKPIVFSDDGRVKDDDTLIFENYRADMRQICEC 272
 Database 49 LGSMDFMPKTSQIMKERRQTEFTSGVTTICPSSRSTILG-LVYNNHHVTNNQ--NC 104

Query 273 IGLERVKDNLSSVPSPHKNIQI-----SGMTOQYNEKEPPFPSSUFPPTHTNVLAELWA 323
 Database 105 TGVENRK----VHEKSIGVYQLQERAGYRTAYLGKLYLNED-GSYTTP-----146

Query 324 SQGVTOFHCA-TEKYPHVTFFNGRE-----VQFQDEE--RCM 360
 Database 147 -GWDEWHAIVKNSKEYNYTMNSNFERKGSEYEKDYFDLVINRSLKFIDKHIKRAW 204

Query 361 VPSPKEVATYDLK--PEMNAGVAEMVQEIESGRPHPLYMCNFAP-PD--MVGHGTGKE 414
 Database 205 QPFAL-LISYPAPHGEPDPAQFAMFENEIS---HRTGSWNFAPNPDKWLQRTGKMN 260

Query 415 PA-----YKACQATDEAIGKIF---EACQTYNYVLAVTSSDIGNAERKIAAPDG 458
 Database 261 DVHISSTDLLHRRRLQTLSQSYDGEIRFLNLREQLNQWNTYAITSDHG-----310

Query 459 SEHTAHTCNL---VPTFCSSKTKTFVKSTP-PTGDGKERAALRDVAPTVLQLMGLPV 512
 Database 311 -YHLGCFGLLKGNMMEYEFDIRVPPFMRGPSIPRNVTFNELTVNY-DIAPTMHLTAGVPK 368

Query 513 PPEMDGVPLLE 523
 Database 369 PARMNRSLLE 379

RESULT 10
 US-08-445-586-2
 ; Sequence 7, Application US/08445586
 ; Patent No. 5627050
 ; GENERAL INFORMATION:
 ; APPLICANT: Taleshita, Sunao
 ; ADDRESS: Ito, Toshimi
 ; APPLICANT: Otarawa-Hamamoto, Yoko
 ; APPLICANT: Amann, Egon
 ; TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and
 ; PROCESS FOR ITS PRODUCTION
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; PRIORITY APPLICATION NUMBER: US/08/445,586
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/111,887
 ; FILING DATE: 26-AUG-1993
 ; APPLICATION NUMBER: JP 230030/92
 ; FILING DATE: 28-AUG-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 324034/92
 ; FILING DATE: 03-DEC-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Forman, David S.

REGISTRATION NUMBER: 33,694
 REFERENCE/DOCKET NUMBER: 024-81-1322-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEX/FAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 556 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-445-586-2

Query Match Score 108; DB 1; Length 556;
 Best Local Similarity 19.4%; Pred. No. 0.0094;
 Matches 75; Conservative 43; Mismatches 100; Indels 168; Gaps 19;

REF ID: QY177

Query 177 SEKYGELATITGRYYAMDRDKRWER----TKMAYEAIVGGIGQK-----ATVDK 221
 Database 126 TQKFGKVDTYSGHHSISNRVEAWTRDVAFLLRQEGRPIINLIPDKNRRRVMTKDQNTDK 185

Query 222 AVDVYERYAQSETDEFLKPIVFSDDGRVKDDDTLIFENYRADMRQICBCLGLERYKDL 281
 Database 186 AEWLRQ-----YNYTKPEVL-----YLGL 205

Query 282 NSVPHPKNTIQISGMQTQYNKEFPPSPL--FPVPT-HTVNLAEWLASQGVTFQHCAETEK 337
 Database 206 N-LPPIP-----YPSPSGENFGSSFEHTSLSY-WL-----232

Query 338 YPHVTEFFENGGREVQFQDEERCVMVPSPKEVATYDLKPEMNAGVAEMVROIE-SGRHPL 396
 Database 233 -----EKVAYD-----AIKIPKWLTLSQMHPV 254

Query 397 VMCNFAPPDMVGHGTGF-EPRVK-----ACQATDEAIGKIFERACQTYNY-----VLMV 443
 Database 255 DFCSSYTAKNC--TGKFTENIKNTRAFYAMCAEDAMGEITLALKHLDLQRTIVY 311

Query 444 TSDHGNAE-----KMIAPDGSEHTAHTCNLVPFTCSKTFVFKSPTPPGTDGKERARA 496
 Database 312 TSDHGMEMAREHQFKMSMTAHSV-----VPLLMMGPSTKANLQVPS-----VVS 357

Query 497 LRDVAPTVLQLMGLPVPPEMDGVPL 522
 Database 358 LVDIYTMFLDIGITALPPNLGSYSL 383

RESULT 11
 US-08-445-586-7
 ; Sequence 7, Application US/08445586
 ; Patent No. 5627050
 ; GENERAL INFORMATION:
 ; APPLICANT: Takeshita, Sunao
 ; ADDRESS: Ito, Toshimi
 ; APPLICANT: Otarawa-Hamamoto, Yoko
 ; APPLICANT: Amann, Egon
 ; TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and
 ; PROCESS FOR ITS PRODUCTION
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; PRIORITY APPLICATION NUMBER: US/08/445,586
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/111,887
 ; FILING DATE: 26-AUG-1993
 ; APPLICATION NUMBER: JP 230030/92
 ; FILING DATE: 28-AUG-1992
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: JP 324034/92
 ; FILING DATE: 03-DEC-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Forman, David S.

COUNTRY: USA
 ZIP: 20005-3314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/445,586

FILING DATE: CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/111,887
 FILING DATE: 26-AUG-1993
 APPLICATION NUMBER: JP 324034/92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 0-DEC-1992
 FILING DATE: 202-08-4000
 ATTORNEY/AGENT INFORMATION:
 NAME: Forman, David S.
 REGISTRATION NUMBER: 33,694
 REFERENCE DOCKET NUMBER: 02481.1322-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4400
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 554 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-445-586-7

Query Match Score 101; DB 1; Length 554;
 Best Local Similarity 19.1%; Pred. No. 0.057;
 Matches 73; Conservative 43; Mismatches 104; Indels 162; Gaps 19;

| Query | Subject | Score | DB | Length | Local Similarity | Pred. | Mismatches | Indels | Gaps | Matches | Conservative | Topology | Sequence Characteristics | MoLecule Type | Length | | | | |
|-----------|---|-------|---|---------|--|------------------------------------|------------------------------------|------------------|-------------|---|--|----------|--------------------------|---------------|---------------------------|--|------------------------------------|------------------------------------|-------------|
| Qy | 177 SKYGELETATGYYANDRDKRWER----ITMAYENIVGGIGQK-----ATVDK 221 | 3.6% | Db | 9 | 100; | DB 3; | Score 100; | DB 3; | Length 920; | Qy | 111 GSGRHLHLLGLVSD----GVVHSIDHFLALIFAKQLOPKVTFHFFADGRDTSPSGA 165 | 3.6% | Db | 9 | 113,373 | Best Local Similarity 21.6%; Pred. No. 0.18; | APPLICATION NUMBER: US/08/930,996A | APPLICATION NUMBER: US/08/930,996A | Length 920; |
| Db | 126 TQKGKVDTYSFGHSISNRVEAWTRDVAFLRQEGRPLINLPDKNRRVWTKDWONTDK 185 | 22; | Db | 54 | 118; | Gaps 22; | Matches 96; | Conservative 64; | Indels 118; | Db | 166 G----YLGRLQQL-FIASKEK-----YGELETATGYYANDRDKRWERI 202 | 21.6% | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | |
| Qy | 222 AVDVVERRYAQSSETDEFIPLTVFSDDRVKDDTLIFFNYADRMRQICECLGLERYKDL 281 | Qy | 111 GSGRHLHLLGLVSD----GVVHSIDHFLALIFAKQLOPKVTFHFFADGRDTSPSGA 165 | 22; | Db | 54 | 118; | Gaps 22; | Db | 166 G----YLGRLQQL-FIASKEK-----YGELETATGYYANDRDKRWERI 202 | 21.6% | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Db | 186 AELWLQ-----VNYTKPFL-----YLGL 205 | Db | 9 | 113,373 | Best Local Similarity 21.6%; Pred. No. 0.18; | APPLICATION NUMBER: US/08/930,996A | APPLICATION NUMBER: US/08/930,996A | Length 920; | Qy | 167 MWARHSIAQKLGVNVNMQSISDSMKRYHSNTYQAAUPLPI---DGDOAKWNINSESS 163 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Qy | 282 NSSVSPHPKNIQISGMTOYKNERPFSI--FPFPVT-HTNVLAEMLASQGTQFHCACTEK 337 | Db | 54 | 118; | Gaps 22; | Matches 96; | Conservative 64; | Indels 118; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Db | 206 N----PHP-----YPSPSGGENGSSTFTHSLY--WL-----231 | Db | 54 | 118; | Gaps 22; | Matches 96; | Conservative 64; | Indels 118; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Qy | 338 VPHYEFFNGGREVOFDEERCMVPSPKEVATYDLKEMNAAGVAKMVEQLE-SGRHPL 396 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Db | 232 -----EKYAYD-----AIKPKWLTLSQHHPV 253 | Db | 206 --TTLSANIFKSQSVRR ---HPESYANVVTI ---SKSYVIEDFVRTMKEFKADTQ 254 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Qy | 397 VMCNFAPPDMWHTGKF-EPAVK-----ACQATEDAIGKIFEAQCTQNY---VLMV 443 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Db | 254 DFCSSYTKNC---TGFCTENETKNAFRYYAMCAEDAMIGETILATHKLQLQKTYIV 310 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Qy | 444 TSDHGN--AEKMLAPGSETEHTATCNCVLPPTCSKTEFEVKSTPPTGDKRERALRDV 500 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Db | 311 TSDHGEMAMEHQFYKMSYESVH---VPLLMNGPGIKANLQVPS-----VVSLVDI 359 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Qy | 501 APTVLQMLGPVPPPEMDGVPL 522 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| Db | 360 YPTMLDIAGILAPPNLGSYSL 381 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| RESULT 12 | US-08-930-996A-8 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | Sequence 8, Application US/08930996A | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | Patent No. 6100449 | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: FLUHR, Robert | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: ESHER, Yuval | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: ORI, Naomi | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: PARAN, Ilan | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: ZAMIR, Daniel | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: WALTER, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | GENERAL INFORMATION: | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: HALL, T. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | 118; | Gaps 22; | Db | 203 KMAYEATNGIGQKATVDKAVDVYREPYKAQSETDE-FLKPKIVFSDGPKV----DDPDI 256 | 22; | Db | 54 | 118; | SEQUENCE CHARACTERISTICS: | SEQUENCE CHARACTERISTICS: | Length 920; | | |
| | APPLICANT: RUBENFELD, et al. | Qy | 257 IFFNYRADMNRQICECLGLERYKD----LNNSVPHPKNQISGMNTQYKEPPFSLFPP 311 | 22; | Db | 54 | | | | | | | | | | | | | |

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIORITY APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 28031
LENGTH: 376
TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*
US-09-252,991A-28031

Query Match Score 98: DB 4; Length 376;
Best Local Similarity 21.28%; Pred. No. 0.062; Indels 58; Gaps 8;
Matches 49; Conservative 34; Mismatches 90; Indels 58; Gaps 8;

Qy 18 GWGLSIDEQHGNAIAKAKTPIMDKLCGNNWQKLEANGLHVGLPEGLMGNSEVGHLNIGAGR 77
Db 85 GAGLACQHRRFAGRATT-----GAALDFQAGRGTDEVAEAVIG--- 124

Qy 78 VIYQDVIRINIAVQRBEVTNPQIVSAERAK-----KGSGRHLHLGLIVSDGGVHSHTI 130
Db 125 -----LARLQLRAGRCOFALHAQVAGHQRRORTQVEQGEADGADHFAGVVVDRAHHH- 178

Qy 131 DHLFLATJTRAFQKLVQPFVTFADGRDTSPSTSGAGCYLEQOLLQFTASEKYG----- 181
Db 179 --QRVLRAIHVHQDRLAAVHLAQATGDHFAGPADSLURVEAEUTGVVALDPDDA 235

Qy 182 ELATITGRRYY--MORDKMRERIKMAYEAIVGGIGQKATYDKAIVYVRER 229
Db 236 GLAVDHRAFGADEFDLEQRTDRLLAYALV-----ILEAVGVHRR 276

RESULT 14
US-08-657-392-2
Sequence 2, Application US/08657392

GENERAL INFORMATION:
APPLICANT: Brate, E.M.
APPLICANT: Brennan, C.A.
APPLICANT: Bridon, D.P.
APPLICANT: Jaffee, K.D.
APPLICANT: Kraft, G.A.
APPLICANT: Mandicki, W.
APPLICANT: March, S.C.
APPLICANT: Russell, J.R.
APPLICANT: Yue, V.T.

TITLE OF INVENTION: Genetically Engineered Enzymes And Their
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: SoftPC

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,392
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/100,708
FILING DATE: JULY 29, 1993
ATTORNEY/AGENT INFORMATION:

NAME: Wong, Wean Khing
REGISTRATION NUMBER: 33,561
REFERENCE/DOCKET NUMBER: 5324.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 938-3517
TELEFAX: (708) 938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acid residues
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM:
US-08-657-392-2

Query Match Score 95: DB 2; Length 449;
Best Local Similarity 18.38%; Pred. No. 0.18; Mismatches 52; Indels 168; Gaps 19;
Matches 90; Conservative 52; Mismatches 183; Indels 168; Gaps 19;

Qy 99 PQIVASAERAKKGSGRHLHLGLIVSDGGVHSHTIKFHFFADGR- 157
Db 2 PEMPVLENRAAQGD-----ITAPOGARRLTGDQTAAALRDSLSDPKAKNTILLGDGMG 54

Qy 158 DTSPSTSGAGCYLEQOLLQFTASEKYG-----YAMDRO-----KRWER 201
Db 55 DSEITAARNYAEGAGFFF--KGIDALPJRQSYTHALNKKTGPDPYVTDSSAASATAWST 111

Qy 202 IKMAYEAVIG-----GIG-----QKATYDKAIVYVRER-YAQ 232
Db 112 GVKTYNGALGYDTHEKDHPHTLEMAKAAGLATGNYSTAELDATPAALVAHTSRSCYGP 171

Qy 233 SETDEFLKPIVYFSDDGRVKDDDLIFFNRYAD-----RMRQIC 270
Db 172 SATSEKCPGNALEKGSKGSITEQLL--NARADVTLGGAKTFAETATAGEQGKTLREQA 229
Qy 271 ECLGLERYKDUNNSVPHPKNTQISGTYQINKEFPFSSLFPVPTHTNLVAENLASQCVTQF 330
Db 230 QARGYQLVSDAAS-----LNSVTEANQOKPLIGF---ADGMPMPVRMLG----- 270

Qy 331 HOAEETKYPHVTEFFNGGREVOFODEERCMYPSPKVEATYDLPKEMN----AAGVAEKM 385
Db 271 -----PRATYHGN-----IDKPAVCTPNPQRNDSVTPLAQNTDKA 306

Qy 386 VEQIESGRHP-IVMCFNAPPDMVHTGKFEPAVAKACQATDEAIGKIFE-ACQTYNVLMV 443
Db 307 TELLSKNEKGFFLQVEGASTIQODHAAANPCCGIGETYVLDLRAVORALEFANKEGNTLV 366

Qy 444 TSDHGNAEKMTAP-----DGSENTA-----HT 465
Db 367 TADHANIASQTVAPDTKAPGLTQALNTKDGAVYMSYGNSEEDSQENTGSQRLIAAYGPHA 426

Qy 466 CNLVPEPICSSKF 478
Db 427 ANVGLTDQTDIF 439

RESULT 15
PCT-U94-02539-2
Sequence 2, Application PC/TUS9402539
GENERAL INFORMATION:
APPLICANT: Brate, E.M.
APPLICANT: Brennan, C.A.
APPLICANT: Bridon, D.P.
APPLICANT: Jaffie, K.D.
APPLICANT: Kraft, G.A.
APPLICANT: Mandicki, W.
APPLICANT: March, S.C.
APPLICANT: Russell, J.R.
APPLICANT: Yue, V.T.

TITLE OF INVENTION: And Their Conjugates For Diagnostic Assays Qy 466 CNLVPFCCSKTF 478
 NUMBER OF INVENTION: 34 Db 427 ANYGLTDQFDLF 439
 CORRESPONDENCE ADDRESS:
 ADDRESSE: ABBOTT LABORATORIES
 STREET: One Abbott Park Road
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: SoftPC
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/02539
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wong, Wean Khing
 REGISTRATION NUMBER: 33-561
 REFERENCE/DOCKET NUMBER: 5324-PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (708) 938-3517
 TELEFAX: (708) 938-2623
 TELEX:
 CLASSIFICATION:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 449 amino acid residues
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM:
 PCT-US94-02539-2

Query Match 3.4%; Score 95; DB 5; Length 449;
 Best Local Similarity 18.3%; Pred. No. 0.18; Matches 90; Conservative 52; Mismatches 183; Indels 168; Gaps 19;

| | | |
|--------|---|---------------------------------|
| Qy 99 | PQIVASAERAKGSGRHLHLGLVSGVSHIDHLFALTRAFKQLQPKVFTHFFADGR- | 157 |
| Db 2 | PMPVLENRAAQQD-----ITAPGARRLTGDOTAALRDSLSDKPAKNILLIGDMG | 54 |
| Qy 158 | DTSPTSGAGYLEQOLLQFIASEKYGELATITGRY-YAMDRD----- | KRWER 201 |
| Db 55 | DSEITAARNYAEGGFF--KGIDALPLTGQTYHYALNKKTGPDPYVTDASAATAWST | 111 |
| Qy 202 | IKMAYEATIG-----GIG----- | -QKATVDAVDDVRR-YAQ 232 |
| Db 112 | GVKTYNGAIGVDIHKDHTITLEMAKAGLATGNVSTAELQDATPAALVAHTTSRKYGP | 171 |
| Qy 233 | SETDEFRLPIVFSDFDRYKDDDTLIFFRYRAD----- | -RMROIC 270 |
| Db 172 | SAYSEKCPGNALEKGKGSITEQLL-NARADYTLGGAKTKFAETATAEWQCKTLEQAA | 229 |
| Qy 271 | ECGLGLEYRKDLNNSSVPHPKNIQISGMQTQYNKEPFPSPFPPYVTHTNNVLAENWLASQGYTQF | 330 |
| Db 230 | QARYQLYSDAAS-----LNSVTEANQKRPPLGLF--ADGNMPVRWLG----- | 270 |
| Qy 331 | HCAETEKYPHVTFNGGREVQFQDERCVMPSPKPEAVYDLPKEMN-----AAGVAEKMK | 385 |
| Db 271 | -----PKATVHG----- | -LDKPAVTCTPNPQRNDSVPLAQMDKA 306 |
| Qy 386 | VEQTESGRP-LVWCNFAPPDMVGHTRGEPAYKACQATDEATGKIFF-ACOTYNYFLMV | 443 |
| Db 307 | IELLSNEKGFFLQVEGASIDKODHAAPCGQIGETVLDDEAVORALEFAKEGNTLVIV | 366 |
| Qy 444 | TSDHGNAEKMIAP----- | -DSEHTA-HT 465 |
| Db 367 | TADHAHASOIVADTKAPGLTOALNTIDGAVMVMSYGNSEEDSQEHRNGSQLRTAAYSPHA | 426 |